



#9
COPY OF PAPERS
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SEQUENCE LISTING

<110> Macrozyme
Aerts, Johannes M.F.G.
Boot, Rolf G.

<120> A mammalian mucinase, its recombinant production, and
its use in therapy or prophylaxis against diseases in
which mucus is involved or infection diseases

<130> 2183-5136US

<140> 10/004,219

<141> 2001-11-02

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human AMCase
amino acid sequence deduced from cDNA sequence

<400> 1

Met Thr Lys Leu Ile Leu Leu Thr Gly Leu Val Leu Ile Leu Asn Leu
1 5 10 15

Gln Leu Gly Ser Ala Tyr Gln Leu Thr Cys Tyr Phe Thr Asn Trp Ala
20 25 30

Gln Tyr Arg Pro Gly Leu Gly Arg Phe Met Pro Asp Asn Ile Asp Pro
35 40 45

Cys Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Arg Gln Asn Asn
50 55 60

Glu Ile Thr Thr Ile Glu Trp Asn Asp Val Thr Leu Tyr Gln Ala Phe
65 70 75 80

Asn Gly Leu Lys Asn Lys Asn Ser Gln Leu Lys Thr Leu Leu Ala Ile
85 90 95

Gly Gly Trp Asn Phe Gly Thr Ala Pro Phe Thr Ala Met Val Ser Thr
100 105 110

Pro Glu Asn Arg Gln Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg
115 120 125

Gln Tyr Glu Phe Asp Gly Leu Asp Phe Asp Trp Glu Tyr Pro Gly Ser
130 135 140

Arg Gly Ser Pro Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Gln
145 150 155 160

Glu Met Arg Glu Ala Phe Glu Gln Glu Ala Lys Gln Ile Asn Lys Pro
165 170 175

Arg Leu Met Val Thr Ala Ala Val Ala Ala Gly Ile Ser Asn Ile Gln
 180 185 190
 Ser Gly Tyr Glu Ile Pro Gln Leu Ser Gln Tyr Leu Asp Tyr Ile His
 195 200 205
 Val Met Thr Tyr Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu
 210 215 220
 Asn Ser Pro Leu Tyr Lys Tyr Pro Thr Asp Thr Gly Ser Asn Ala Tyr
 225 230 235 240
 Leu Asn Val Asp Tyr Val Met Asn Tyr Trp Lys Asp Asn Gly Ala Pro
 245 250 255
 Ala Glu Lys Leu Ile Val Gly Phe Pro Thr Tyr Gly His Asn Phe Ile
 260 265 270
 Leu Ser Asn Pro Ser Asn Thr Gly Ile Gly Ala Pro Thr Ser Gly Ala
 275 280 285
 Gly Pro Ala Gly Pro Tyr Ala Lys Glu Ser Gly Ile Trp Ala Tyr Tyr
 290 295 300
 Glu Ile Cys Thr Phe Leu Lys Asn Gly Ala Thr Gln Gly Trp Asp Ala
 305 310 315 320
 Pro Gln Glu Val Pro Tyr Ala Tyr Gln Gly Asn Val Trp Val Gly Tyr
 325 330 335
 Asp Asn Ile Lys Ser Phe Asp Ile Lys Ala Gln Trp Leu Lys His Asn
 340 345 350
 Lys Phe Gly Gly Ala Met Val Trp Ala Ile Asp Leu Asp Asp Phe Thr
 355 360 365
 Gly Thr Phe Cys Asn Gln Gly Lys Phe Pro Leu Ile Ser Thr Leu Lys
 370 375 380
 Lys Ala Leu Gly Leu Gln Ser Ala Ser Cys Thr Ala Pro Ala Gln Pro
 385 390 395 400
 Ile Glu Pro Ile Thr Ala Ala Pro Ser Gly Ser Gly Asn Gly Ser Gly
 405 410 415
 Ser Ser Ser Ser Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Val
 420 425 430
 Arg Ala Asn Gly Leu Tyr Pro Val Ala Asn Asn Arg Asn Ala Phe Trp
 435 440 445
 His Cys Val Asn Gly Val Thr Tyr Gln Gln Asn Cys Gln Ala Gly Leu
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 Val Phe Asp Thr Ser Cys Asp Cys Cys Asn Trp Ala
 465 470 475

<210> 2
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<223> Description of Combined DNA/RNA Molecule: human
 AMCase cDNA sequence and deduced amino acid
 sequence

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<223> Description of Artificial Sequence: human AMCase
 cDNA sequence and deduced amino acid sequence

<220>

<221> CDS

<222> (104)..(1531)

<400> 2

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                                     Met Thr Lys Leu
                                     1

att ctc ctc aca ggt ctt gtc ctt ata ctg aat ttg cag ctc ggc tct 163
Ile Leu Leu Thr Gly Leu Val Leu Ile Leu Asn Leu Gln Leu Gly Ser
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gcc tac cag ctg aca tgc tac ttc acc aac tgg gcc cag tac cgg cca 211
Ala Tyr Gln Leu Thr Cys Tyr Phe Thr Asn Trp Ala Gln Tyr Arg Pro
                      25                      30                      35

ggc ctg ggg cgc ttc atg cct gac aac atc gac ccc tgc ctc tgt acc 259
Gly Leu Gly Arg Phe Met Pro Asp Asn Ile Asp Pro Cys Leu Cys Thr
                      40                      45                      50

cac ctg atc tac gcc ttt gct ggg agg cag aac aac gag atc acc acc 307
His Leu Ile Tyr Ala Phe Ala Gly Arg Gln Asn Asn Glu Ile Thr Thr
                      55                      60                      65

atc gaa tgg aac gat gtg act ctc tac caa gct ttc aat ggc ctg aaa 355
Ile Glu Trp Asn Asp Val Thr Leu Tyr Gln Ala Phe Asn Gly Leu Lys
                      70                      75                      80

aat aag aac agc cag ctg aaa act ctc ctg gcc att gga ggc tgg aac 403
Asn Lys Asn Ser Gln Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn
                      85                      90                      95                      100

ttc ggg act gcc cct ttc act gcc atg gtt tct act cct gag aac cgc 451
Phe Gly Thr Ala Pro Phe Thr Ala Met Val Ser Thr Pro Glu Asn Arg
                      105                      110                      115

cag act ttc atc acc tca gtc atc aaa ttc ctg cgc cag tat gag ttt 499
Gln Thr Phe Thr Thr Ser Val Ile Lys Phe Leu Arg Gln Tyr Glu Phe
                      120                      125                      130

gac ggg ctg gac ttt gac tgg gag tac cct ggc tct cgt ggg agc cct 547
Asp Gly Leu Asp Phe Asp Trp Glu Tyr Pro Gly Ser Arg Gly Ser Pro
                      135                      140                      145

cct cag gac aag cat ctc ttc act gtc ctg gtg cag gaa atg cgt gaa 595
Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Gln Glu Met Arg Glu

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gct ttt gag cag gag gcc aag cag atc aac aag ccc agg ctg atg gtc Ala Phe Glu Gln Glu Ala Lys Gln Ile Asn Lys Pro Arg Leu Met Val 165 170 175 180			643
act gct gca gta gct gct ggc atc tcc aat atc cag tct ggc tat gag Thr Ala Ala Val Ala Ala Gly Ile Ser Asn Ile Gln Ser Gly Tyr Glu 185 190 195			691
atc ccc caa ctg tca cag tac ctg gac tac atc cat gtc atg acc tac Ile Pro Gln Leu Ser Gln Tyr Leu Asp Tyr Ile His Val Met Thr Tyr 200 205 210			739
gac ctc cat ggc tcc tgg gag ggc tac act gga gag aac agc ccc ctc Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu Asn Ser Pro Leu 215 220 225			787
tac aaa tac ccg act gac acc ggc agc aac gcc tac ctc aat gtg gat Tyr Lys Tyr Pro Thr Asp Thr Gly Ser Asn Ala Tyr Leu Asn Val Asp 230 235 240			835
tat gtc atg aac tac tgg aag gac aat gga gca cca gct gag aag ctc Tyr Val Met Asn Tyr Trp Lys Asp Asn Gly Ala Pro Ala Glu Lys Leu 245 250 255 260			883
atc gtt gga ttc cct acc tat gga cac aac ttc atc ctg agc aac ccc Ile Val Gly Phe Pro Thr Tyr Gly His Asn Phe Ile Leu Ser Asn Pro 265 270 275			931
tcc aac act gga att ggt gcc ccc acc tct ggt gct ggt cct gct ggg Ser Asn Thr Gly Ile Gly Ala Pro Thr Ser Gly Ala Gly Pro Ala Gly 280 285 290			979
ccc tat gcc aag gag tct ggg atc tgg gct tac tac gag atc tgt acc Pro Tyr Ala Lys Glu Ser Gly Ile Trp Ala Tyr Tyr Glu Ile Cys Thr 295 300 305			1027
ttc ctg aaa aat gga gcc act cag gga tgg gat gcc cct cag gaa gtg Phe Leu Lys Asn Gly Ala Thr Gln Gly Trp Asp Ala Pro Gln Glu Val 310 315 320			1075
cct tat gcc tat cag ggc aat gtg tgg gtt ggc tat gac aac atc aag Pro Tyr Ala Tyr Gln Gly Asn Val Trp Val Gly Tyr Asp Asn Ile Lys 325 330 335 340			1123
agc ttc gat att aag gct caa tgg ctt aag cac aac aaa ttt gga ggc Ser Phe Asp Ile Lys Ala Gln Trp Leu Lys His Asn Lys Phe Gly Gly 345 350 355			1171
gcc atg gtc tgg gcc att gat ctg gat gac ttc act ggc act ttc tgc Ala Met Val Trp Ala Ile Asp Leu Asp Asp Phe Thr Gly Thr Phe Cys 360 365 370			1219
aac cag ggc aag ttt ccc cta atc tcc acc ctg aag aag gcc ctc ggc Asn Gln Gly Lys Phe Pro Leu Ile Ser Thr Leu Lys Lys Ala Leu Gly 375 380 385			1267
ctg cag agt gca agt tgc acg gct cca gct cag ccc att gag cca ata Leu Gln Ser Ala Ser Cys Thr Ala Pro Ala Gln Pro Ile Glu Pro Ile 390 395 400			1315

act gct gct ccc agt ggc agc ggg aac ggg agc ggg agt agc agc tct 1363
 Thr Ala Ala Pro Ser Gly Ser Gly Asn Gly Ser Gly Ser Ser Ser
 405 410 415 420

gga ggc agc tcg gga ggc agt gga ttc tgt gct gtc aga gcc aac ggc 1411
 Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Val Arg Ala Asn Gly
 425 430 435

ctc tac ccc gtg gca aat aac aga aat gcc ttc tgg cac tgc gtg aat 1459
 Leu Tyr Pro Val Ala Asn Asn Arg Asn Ala Phe Trp His Cys Val Asn
 440 445 450

gga gtc acg tac cag cag aac tgc cag gcc ggg ctt gtc ttc gac acc 1507
 Gly Val Thr Tyr Gln Gln Asn Cys Gln Ala Gly Leu Val Phe Asp Thr
 455 460 465

agc tgt gat tgc tgc aac tgg gca taaacctgac ctggtctata ttccctagag 1561
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agtc 1625

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<220>
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 AMCase cDNA sequence and deduced amino acid
 sequence

<220>
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 cDNA sequence and deduced amino acid sequence

<220>
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 <222> (1)..(1419)

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 1 5 10 15

cag ctg ggg tct gcc tac aat ctg ata tgc tat ttc acc aac tgg gcc 96
 Gln Leu Gly Ser Ala Tyr Asn Leu Ile Cys Tyr Phe Thr Asn Trp Ala
 20 25 30

cag tat cgg cca ggt ctg ggg agc ttc aag cct gat gac att aac ccc 144
 Gln Tyr Arg Pro Gly Leu Gly Ser Phe Lys Pro Asp Asp Ile Asn Pro
 35 40 45

tgc ctg tgt act cac ctg atc tat gcc ttt gct ggg atg cag aac aat 192
 Cys Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Gln Asn Asn
 50 55 60

gag atc acc acc ata gaa tgg aat gat gtt act ctc tat aaa gct ttc	240
Glu Ile Thr Thr Ile Glu Trp Asn Asp Val Thr Leu Tyr Lys Ala Phe	
65 70 75 80	
aat gac ttg aaa aac agg aac agc aaa ctg aaa acc ctc ctg gca att	288
Asn Asp Leu Lys Asn Arg Asn Ser Lys Leu Lys Thr Leu Leu Ala Ile	
85 90 95	
gga ggc tgg aac ttt gga act gct cct ttc act acc atg gtt tcc act	336
Gly Gly Trp Asn Phe Gly Thr Ala Pro Phe Thr Thr Met Val Ser Thr	
100 105 110	
tct cag aac cgc cag acc ttc att acc tca gtc atc aaa ttt ctg cgt	384
Ser Gln Asn Arg Gln Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg	
115 120 125	
cag tat ggg ttt gat gga ctg gac ctg gac tgg gaa tac cca ggc tca	432
Gln Tyr Gly Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser	
130 135 140	
cgt ggg agc cct cct cag gac aag cat ctc ttc act gtc ctg gtg aag	480
Arg Gly Ser Pro Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Lys	
145 150 155 160	
gaa atg cgt gaa gct ttt gag cag gag gct att gag agc aac agg ccc	528
Glu Met Arg Glu Ala Phe Glu Gln Glu Ala Ile Glu Ser Asn Arg Pro	
165 170 175	
aga ctg atg gtt act gct gct gta gct ggt ggg att tcc aac atc cag	576
Arg Leu Met Val Thr Ala Ala Val Ala Gly Gly Ile Ser Asn Ile Gln	
180 185 190	
gct ggc tat gag atc cct gaa ctt tct aag tac ctg gat ttc atc cat	624
Ala Gly Tyr Glu Ile Pro Glu Leu Ser Lys Tyr Leu Asp Phe Ile His	
195 200 205	
gtc atg aca tat gac ctc cat ggc tcc tgg gag ggc tac act ggg gag	672
Val Met Thr Tyr Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu	
210 215 220	
aat agt cct ctt tac aaa tac cct act gag act ggt agc aat gcc tac	720
Asn Ser Pro Leu Tyr Lys Tyr Pro Thr Glu Thr Gly Ser Asn Ala Tyr	
225 230 235 240	
ctc aat gtg gat tat gtc atg aac tat tgg aag aac aat gga gcc cca	768
Leu Asn Val Asp Tyr Val Met Asn Tyr Trp Lys Asn Asn Gly Ala Pro	
245 250 255	
gct gag aag ctc att gtt gga ttc cca gag tat gga cac acc ttc atc	816
Ala Glu Lys Leu Ile Val Gly Phe Pro Glu Tyr Gly His Thr Phe Ile	
260 265 270	
ctg aga aac ccc tct gat aat gga att ggt gcc cct acc tct ggt gat	864
Leu Arg Asn Pro Ser Asp Asn Gly Ile Gly Ala Pro Thr Ser Gly Asp	
275 280 285	
ggc cct gct ggc gcc tat acc aga cag gct ggg ttc tgg gcc tac tat	912
Gly Pro Ala Gly Ala Tyr Thr Arg Gln Ala Gly Phe Trp Ala Tyr Tyr	
290 295 300	
gag att tgc acc ttt ctg aga agt gga gcc act gag gtc tgg gat gcc	960

Gln Leu Gly Ser Ala Tyr Asn Leu Ile Cys Tyr Phe Thr Asn Trp Ala
 20 25 30

Gln Tyr Arg Pro Gly Leu Gly Ser Phe Lys Pro Asp Asp Ile Asn Pro
 35 40 45

Cys Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Gln Asn Asn
 50 55 60

Glu Ile Thr Thr Ile Glu Trp Asn Asp Val Thr Leu Tyr Lys Ala Phe
 65 70 75 80

Asn Asp Leu Lys Asn Arg Asn Ser Lys Leu Lys Thr Leu Leu Ala Ile
 85 90 95

Gly Gly Trp Asn Phe Gly Thr Ala Pro Phe Thr Thr Met Val Ser Thr
 100 105 110

Ser Gln Asn Arg Gln Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg
 115 120 125

Gln Tyr Gly Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser
 130 135 140

Arg Gly Ser Pro Pro Gln Asp Lys His Leu Phe Thr Val Leu Val Lys
 145 150 155 160

Glu Met Arg Glu Ala Phe Glu Gln Glu Ala Ile Glu Ser Asn Arg Pro
 165 170 175

Arg Leu Met Val Thr Ala Ala Val Ala Gly Gly Ile Ser Asn Ile Gln
 180 185 190

Ala Gly Tyr Glu Ile Pro Glu Leu Ser Lys Tyr Leu Asp Phe Ile His
 195 200 205

Val Met Thr Tyr Asp Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu
 210 215 220

Asn Ser Pro Leu Tyr Lys Tyr Pro Thr Glu Thr Gly Ser Asn Ala Tyr
 225 230 235 240

Leu Asn Val Asp Tyr Val Met Asn Tyr Trp Lys Asn Asn Gly Ala Pro
 245 250 255

Ala Glu Lys Leu Ile Val Gly Phe Pro Glu Tyr Gly His Thr Phe Ile
 260 265 270

Leu Arg Asn Pro Ser Asp Asn Gly Ile Gly Ala Pro Thr Ser Gly Asp
 275 280 285

Gly Pro Ala Gly Ala Tyr Thr Arg Gln Ala Gly Phe Trp Ala Tyr Tyr
 290 295 300

Glu Ile Cys Thr Phe Leu Arg Ser Gly Ala Thr Glu Val Trp Asp Ala
 305 310 315 320

Ser Gln Glu Val Pro Tyr Ala Tyr Lys Ala Asn Glu Trp Leu Gly Tyr
 325 330 335

Asp Asn Ile Lys Ser Phe Ser Val Lys Ala Gln Trp Leu Lys Gln Asn

340	345	350
Asn Phe Gly Gly Ala Met Ile Trp Ala Ile Asp Leu Asp Asp Phe Thr		
355	360	365
Gly Ser Phe Cys Asp Gln Gly Lys Phe Pro Leu Thr Ser Thr Leu Asn		
370	375	380
Lys Ala Leu Gly Ile Ser Thr Glu Gly Cys Thr Ala Pro Asp Val Pro		
385	390	395
Ser Glu Pro Val Thr Thr Pro Pro Gly Ser Gly Ser Gly Gly Gly Ser		
	405	410
Ser Gly Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Asp Lys Ala Asp		
	420	425
Gly Leu Tyr Pro Val Ala Asp Asp Arg Asn Ala Phe Trp Gln Cys Ile		
	435	440
Asn Gly Ile Thr Tyr Gln Gln His Cys Gln Ala Gly Leu Val Phe Asp		
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Thr Ser Cys Asn Cys Cys Asn Trp Pro		
465	470	

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 <213> Artificial Sequence

<220>
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 <222> (1)..(22)

<400> 5
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<210> 6
 <211> 23
 <212> DNA
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 primer MAS1

<220>
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 <222> (1)..(23)

<400> 6
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<210> 7

<211> 21
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 <213> Artificial Sequence

<220>
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 primer MAS2

<220>
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 <222> (1)..(21)

<400> 7
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21

<210> 8
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: sense primer
 MS1

<220>
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 <222> (1)..(22)

<400> 8
 cgatggccaa gctacttctc gt

22

<210> 9
 <211> 452
 <212> PRT
 <213> Mus musculus

<220>
 <221> SITE
 <222> (1)..(452)
 <223> /note="Mouse AMCase"

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 Leu Gly Ser Phe Lys Pro Asp Asp Ile Asn Pro Cys Leu Cys Thr His
 20 25 30
 Leu Ile Tyr Ala Phe Ala Gly Met Gln Asn Asn Glu Ile Thr Thr Ile
 35 40 45
 Glu Trp Asn Asp Val Thr Leu Tyr Lys Ala Phe Asn Asp Leu Lys Asn
 50 55 60
 Arg Asn Ser Lys Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn Phe
 65 70 75 80
 Gly Thr Ala Pro Phe Thr Thr Met Val Ser Thr Ser Gln Asn Arg Gln
 85 90 95

Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg Gln Tyr Gly Phe Asp
 100 105 110
 Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser Arg Gly Ser Pro Pro
 115 120 125
 Gln Asp Lys His Leu Phe Thr Val Leu Val Lys Glu Met Arg Glu Ala
 130 135 140
 Phe Glu Gln Glu Ala Ile Glu Ser Asn Arg Pro Arg Leu Met Val Thr
 145 150 155 160
 Ala Ala Val Ala Gly Gly Ile Ser Asn Ile Gln Ala Gly Tyr Glu Ile
 165 170 175
 Pro Glu Leu Ser Lys Tyr Leu Asp Phe Ile His Val Met Thr Tyr Asp
 180 185 190
 Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu Asn Ser Pro Leu Tyr
 195 200 205
 Lys Tyr Pro Thr Glu Thr Gly Ser Asn Ala Tyr Leu Asn Val Asp Tyr
 210 215 220
 Val Met Asn Tyr Trp Lys Asn Asn Gly Ala Pro Ala Glu Lys Leu Ile
 225 230 235 240
 Val Gly Phe Pro Glu Tyr Gly His Thr Phe Ile Leu Arg Asn Pro Ser
 245 250 255
 Asp Asn Gly Ile Gly Ala Pro Thr Ser Gly Asp Gly Pro Ala Gly Ala
 260 265 270
 Tyr Thr Arg Gln Ala Gly Phe Trp Ala Tyr Tyr Glu Ile Cys Thr Phe
 275 280 285
 Leu Arg Ser Gly Ala Thr Glu Val Trp Asp Ala Ser Gln Glu Val Pro
 290 295 300
 Tyr Ala Tyr Lys Ala Asn Glu Trp Leu Gly Tyr Asp Asn Ile Lys Ser
 305 310 315 320
 Phe Ser Val Lys Ala Gln Trp Leu Lys Gln Asn Asn Phe Gly Gly Ala
 325 330 335
 Met Ile Trp Ala Ile Asp Leu Asp Asp Phe Thr Gly Ser Phe Cys Asp
 340 345 350
 Gln Gly Lys Phe Pro Leu Thr Ser Thr Leu Asn Lys Ala Leu Gly Ile
 355 360 365
 Ser Thr Glu Gly Cys Thr Ala Pro Asp Val Pro Ser Glu Pro Val Thr
 370 375 380
 Thr Pro Pro Gly Ser Gly Ser Gly Gly Gly Ser Ser Gly Gly Ser Ser
 385 390 395 400
 Gly Gly Ser Gly Phe Cys Ala Asp Lys Ala Asp Gly Leu Tyr Pro Val
 405 410 415

Ala Asp Asp Arg Asn Ala Phe Trp Gln Cys Ile Asn Gly Ile Thr Tyr
 420 425 430

Gln Gln His Cys Gln Ala Gly Leu Val Phe Asp Thr Ser Cys Asn Cys
 435 440 445

Cys Asn Trp Pro
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<210> 10
 <211> 445
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(445)
 <223> /note="Human chitotriosidase"

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 1 5 10 15

Glu Ala Arg Phe Leu Pro Lys Asp Leu Asp Pro Ser Leu Cys Thr His
 20 25 30

Leu Ile Tyr Ala Phe Ala Gly Met Thr Asn His Gln Leu Ser Thr Thr
 35 40 45

Glu Trp Asn Asp Glu Thr Leu Tyr Gln Glu Phe Asn Gly Leu Lys Lys
 50 55 60

Met Asn Pro Lys Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn Phe
 65 70 75 80

Gly Thr Gln Lys Phe Thr Asp Met Val Ala Thr Ala Asn Asn Arg Gln
 85 90 95

Thr Phe Val Asn Ser Ala Ile Arg Phe Leu Arg Lys Tyr Ser Phe Asp
 100 105 110

Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser Gln Gly Ser Pro Ala
 115 120 125

Val Asp Lys Glu Arg Phe Thr Thr Leu Val Gln Asp Leu Ala Asn Ala
 130 135 140

Phe Gln Gln Glu Ala Gln Thr Ser Gly Lys Glu Arg Leu Leu Leu Ser
 145 150 155 160

Ala Ala Val Pro Ala Gly Gln Thr Tyr Val Asp Ala Gly Tyr Glu Val
 165 170 175

Asp Lys Ile Ala Gln Asn Leu Asp Phe Val Asn Leu Met Ala Tyr Asp
 180 185 190

Phe His Gly Ser Trp Glu Lys Val Thr Gly His Asn Ser Pro Leu Tyr
 195 200 205

Lys Arg Gln Glu Glu Ser Gly Ala Ala Ala Ser Leu Asn Val Asp Ala

210	215	220
Ala Val Gln Gln Trp Leu Gln Lys Gly Thr Pro Ala Ser Lys Leu Ile 225 230 235 240		
Leu Gly Met Pro Thr Tyr Gly Arg Ser Phe Thr Leu Ala Ser Ser Ser 245 250 255		
Asp Thr Arg Val Gly Ala Pro Ala Thr Gly Ser Gly Thr Pro Gly Pro 260 265 270		
Phe Thr Lys Glu Gly Gly Met Leu Ala Tyr Tyr Glu Val Cys Ser Trp 275 280 285		
Lys Gly Ala Thr Lys Gln Arg Ile Gln Asp Gln Lys Val Pro Tyr Ile 290 295 300		
Phe Arg Asp Asn Gln Trp Val Gly Phe Asp Asp Val Glu Ser Phe Lys 305 310 315 320		
Thr Lys Val Ser Tyr Leu Lys Gln Lys Gly Leu Gly Gly Ala Met Val 325 330 335		
Trp Ala Leu Asp Leu Asp Asp Phe Ala Gly Phe Ser Cys Asn Gln Gly 340 345 350		
Arg Tyr Pro Leu Ile Gln Thr Leu Arg Gln Glu Leu Ser Leu Pro Tyr 355 360 365		
Leu Pro Ser Gly Thr Pro Glu Leu Glu Val Pro Lys Pro Gly Gln Pro 370 375 380		
Ser Glu Pro Glu His Gly Pro Ser Pro Gly Gln Asp Thr Phe Cys Gln 385 390 395 400		
Gly Lys Ala Asp Gly Leu Tyr Pro Asn Pro Arg Glu Arg Ser Ser Phe 405 410 415		
Tyr Ser Cys Ala Ala Gly Arg Leu Phe Gln Gln Ser Cys Pro Thr Gly 420 425 430		
Leu Val Phe Ser Asn Ser Cys Lys Cys Cys Thr Trp Asn 435 440 445		

<210> 11
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 <212> DNA
 <213> Artificial Sequence

<220>
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<220>
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 <222> (1)..(24)

<400> 11
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 HAS3-A-tail

<220>
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 <222> (1)..(22)

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22

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<220>
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<220>
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 <222> (1)..(22)

<400> 13
 gctttccagt ctggtggtga at

22

<210> 14
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 <213> Homo sapiens

<220>
 <221> SITE
 <222> (1)..(455)
 <223> /note="Human AMCase"

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 20 25 30
 Leu Ile Tyr Ala Phe Ala Gly Arg Gln Asn Asn Glu Ile Thr Thr Ile
 35 40 45
 Glu Trp Asn Asp Val Thr Leu Tyr Gln Ala Phe Asn Gly Leu Lys Asn
 50 55 60
 Lys Asn Ser Gln Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn Phe
 65 70 75 80
 Gly Thr Ala Pro Phe Thr Ala Met Val Ser Thr Pro Glu Asn Arg Gln
 85 90 95

Thr Phe Ile Thr Ser Val Ile Lys Phe Leu Arg Gln Tyr Glu Phe Asp
 100 105 110
 Gly Leu Asp Phe Asp Trp Glu Tyr Pro Gly Ser Arg Gly Ser Pro Pro
 115 120 125
 Gln Asp Lys His Leu Phe Thr Val Leu Val Gln Glu Met Arg Glu Ala
 130 135 140
 Phe Glu Gln Glu Ala Lys Gln Ile Asn Lys Pro Arg Leu Met Val Thr
 145 150 155 160
 Ala Ala Val Ala Ala Gly Ile Ser Asn Ile Gln Ser Gly Tyr Glu Ile
 165 170 175
 Pro Gln Leu Ser Gln Tyr Leu Asp Tyr Ile His Val Met Thr Tyr Asp
 180 185 190
 Leu His Gly Ser Trp Glu Gly Tyr Thr Gly Glu Asn Ser Pro Leu Tyr
 195 200 205
 Lys Tyr Pro Thr Asp Thr Gly Ser Asn Ala Tyr Leu Asn Val Asp Tyr
 210 215 220
 Val Met Asn Tyr Trp Lys Asp Asn Gly Ala Pro Ala Glu Lys Leu Ile
 225 230 235 240
 Val Gly Phe Pro Thr Tyr Gly His Asn Phe Ile Leu Ser Asn Pro Ser
 245 250 255
 Asn Thr Gly Ile Gly Ala Pro Thr Ser Gly Ala Gly Pro Ala Gly Pro
 260 265 270
 Tyr Ala Lys Glu Ser Gly Ile Trp Ala Tyr Tyr Glu Ile Cys Thr Phe
 275 280 285
 Leu Lys Asn Gly Ala Thr Gln Gly Trp Asp Ala Pro Gln Glu Val Pro
 290 295 300
 Tyr Ala Tyr Gln Gly Asn Val Trp Val Gly Tyr Asp Asn Ile Lys Ser
 305 310 315 320
 Phe Asp Ile Lys Ala Gln Trp Leu Lys His Asn Lys Phe Gly Gly Ala
 325 330 335
 Met Val Trp Ala Ile Asp Leu Asp Asp Phe Thr Gly Thr Phe Cys Asn
 340 345 350
 Gln Gly Lys Phe Pro Leu Ile Ser Thr Leu Lys Lys Ala Leu Gly Leu
 355 360 365
 Gln Ser Ala Ser Cys Thr Ala Pro Ala Gln Pro Ile Glu Pro Ile Thr
 370 375 380
 Ala Ala Pro Ser Gly Ser Gly Asn Gly Ser Gly Ser Ser Ser Gly
 385 390 395 400
 Gly Ser Ser Gly Gly Ser Gly Phe Cys Ala Val Arg Ala Asn Gly Leu
 405 410 415

Tyr Pro Val Ala Asn Asn Arg Asn Ala Phe Trp His Cys Val Asn Gly
420 425 430

Val Thr Tyr Gln Gln Asn Cys Gln Ala Gly Leu Val Phe Asp Thr Ser
435 440 445

Cys Asp Cys Cys Asn Trp Ala
450 455